

Figure 1

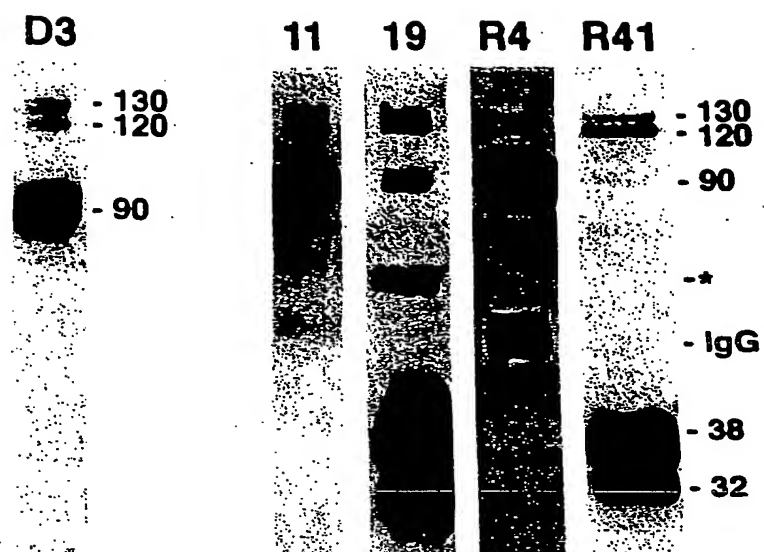


Figure 2A

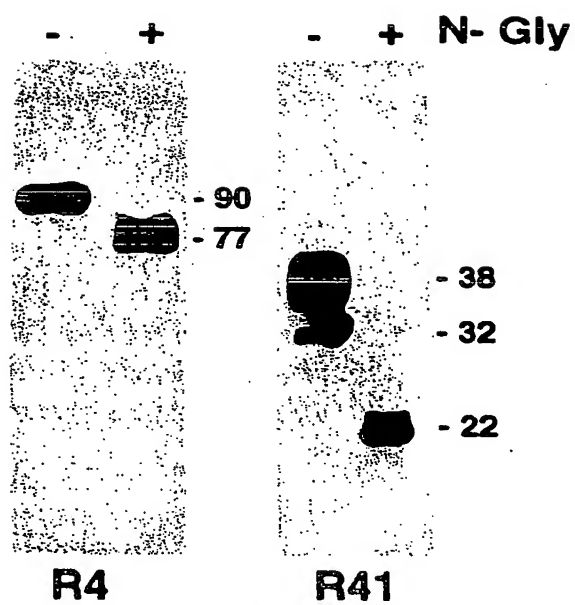


Figure 2B

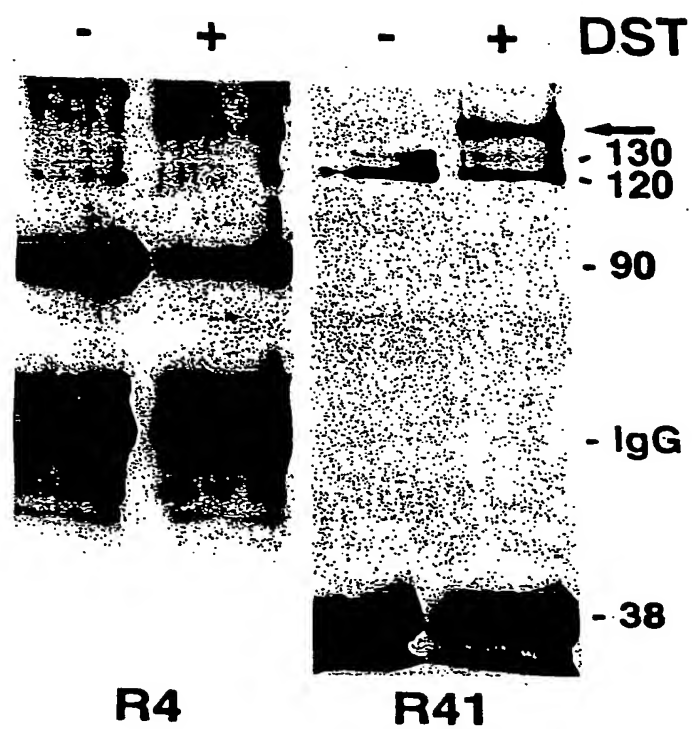


Figure 3A

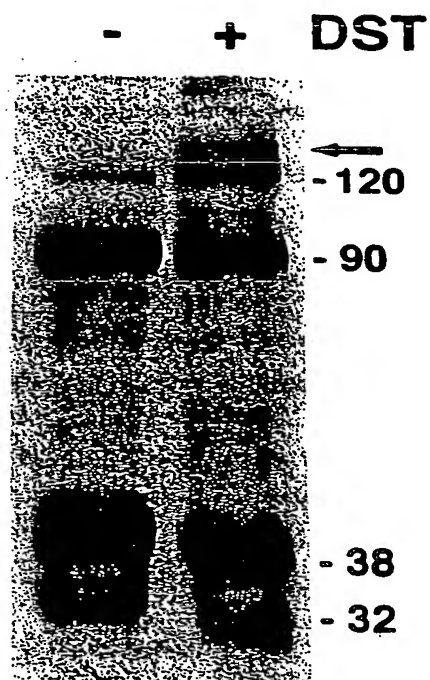


Figure 4A

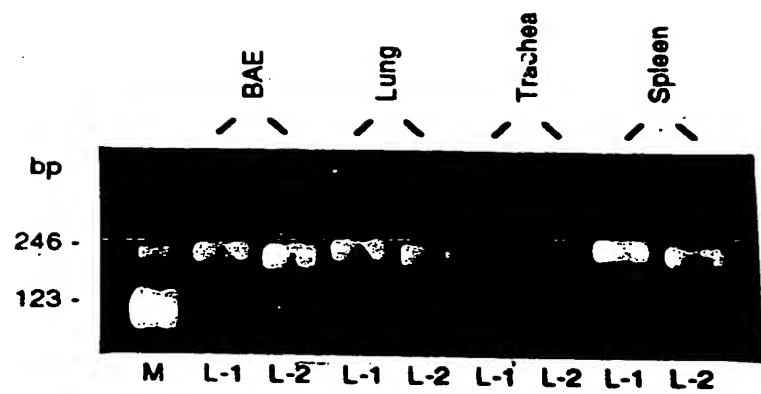
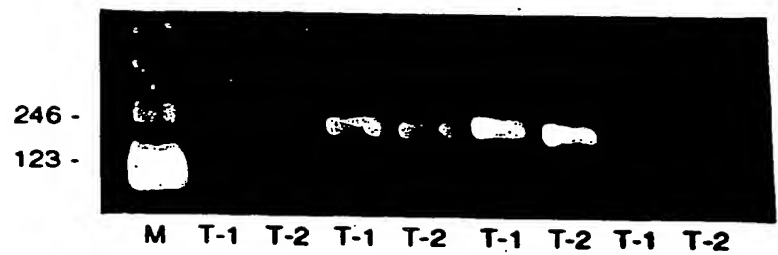


Figure 4B



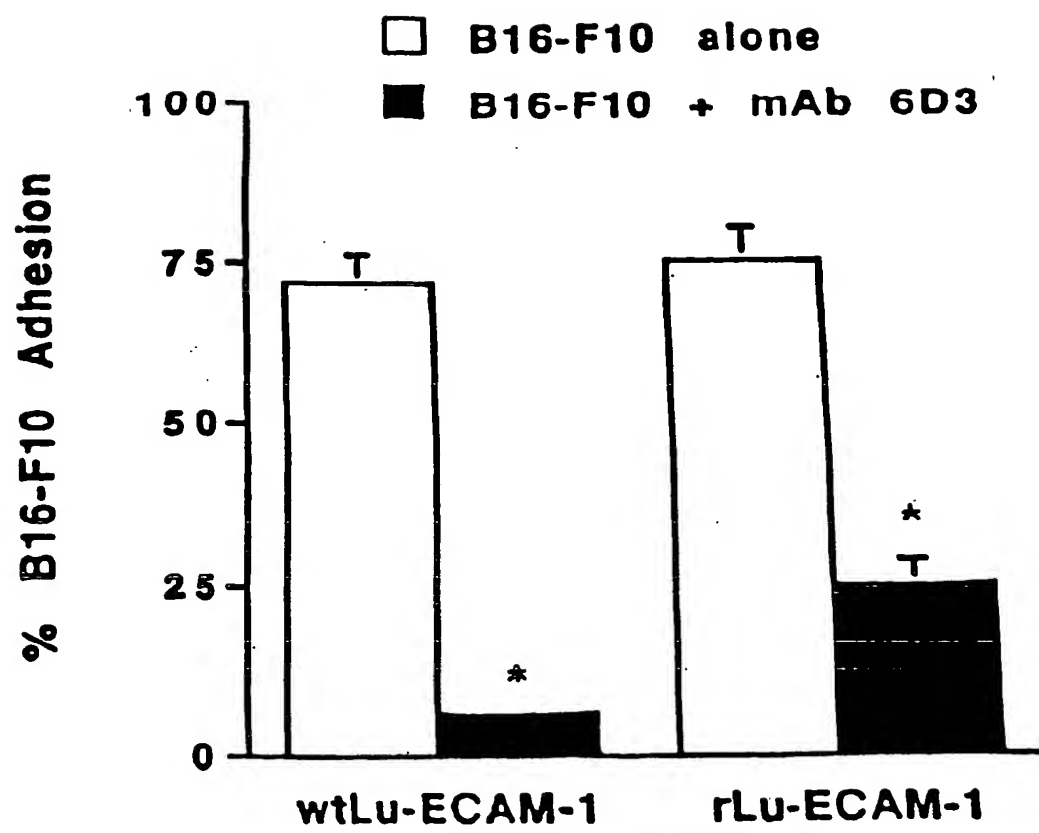


Figure 5

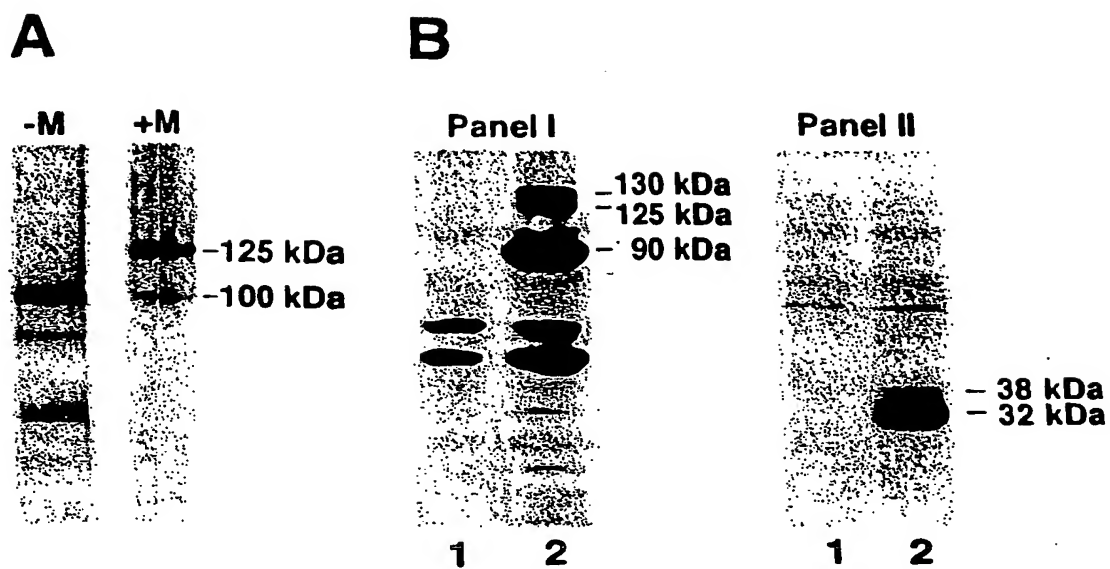


Figure 6

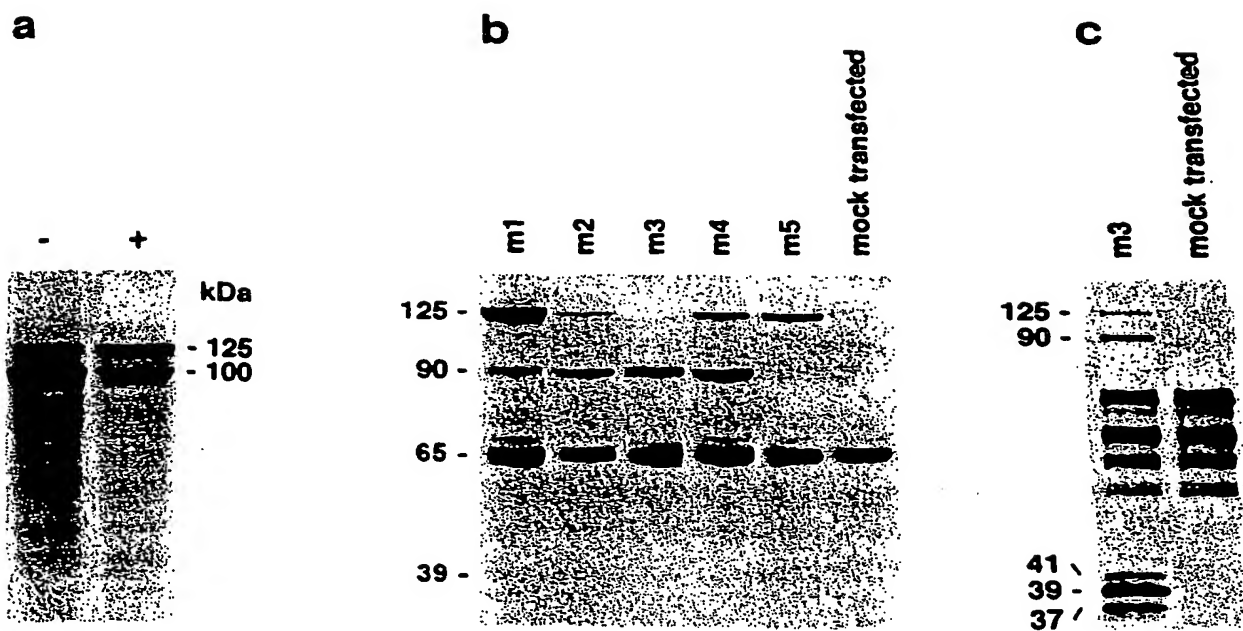


Figure 7

**a**

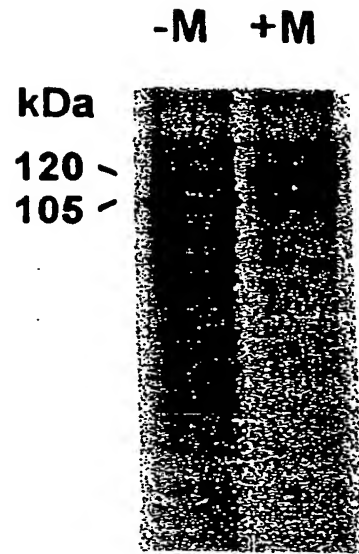
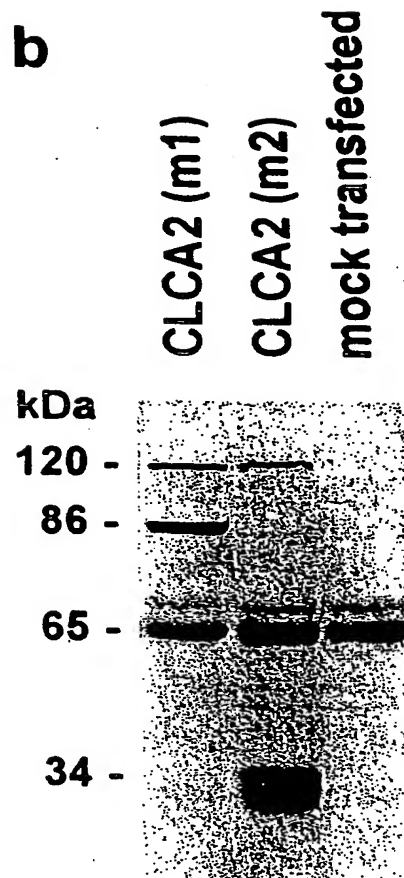


Figure 8

**b**



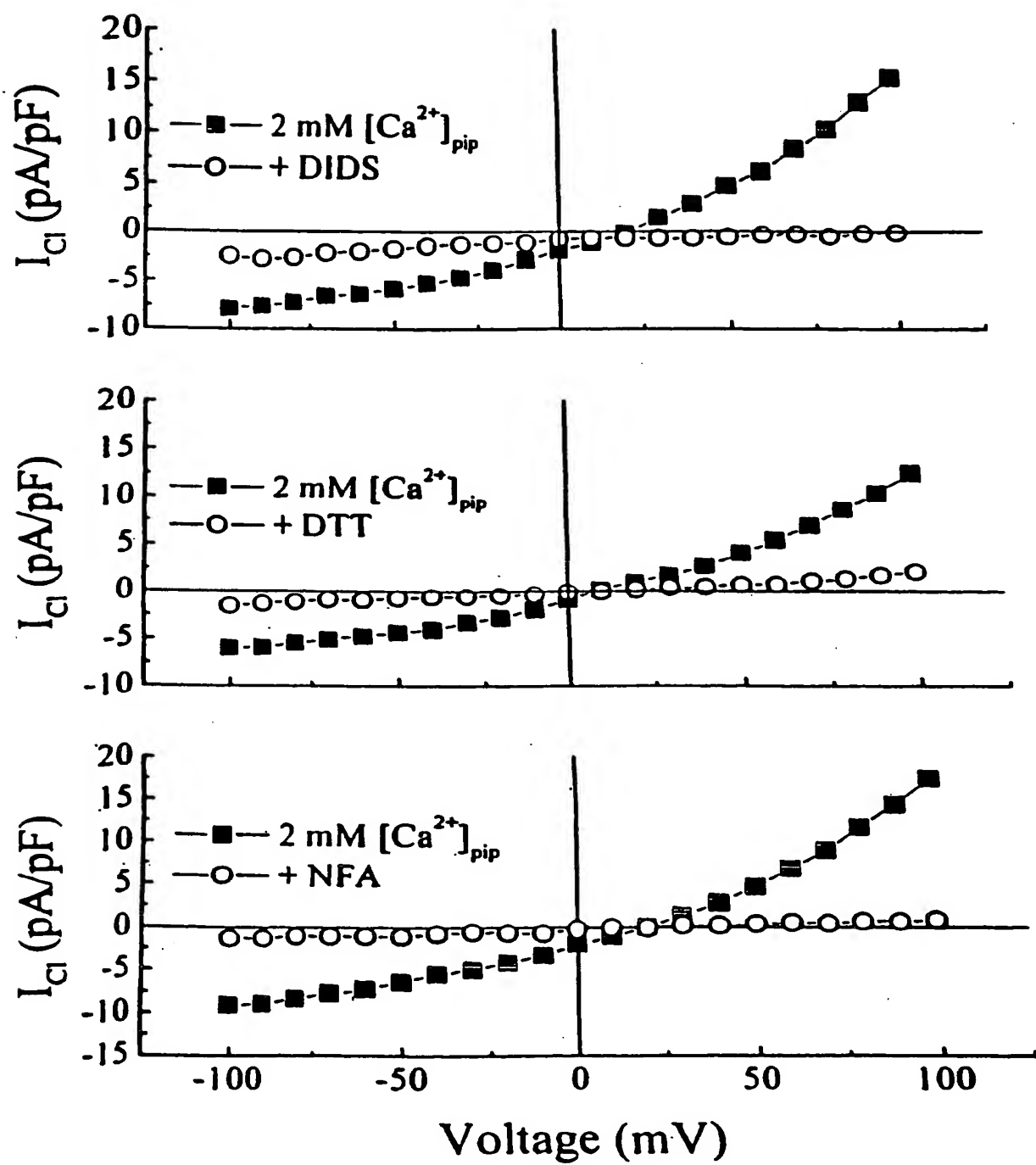


Figure 9



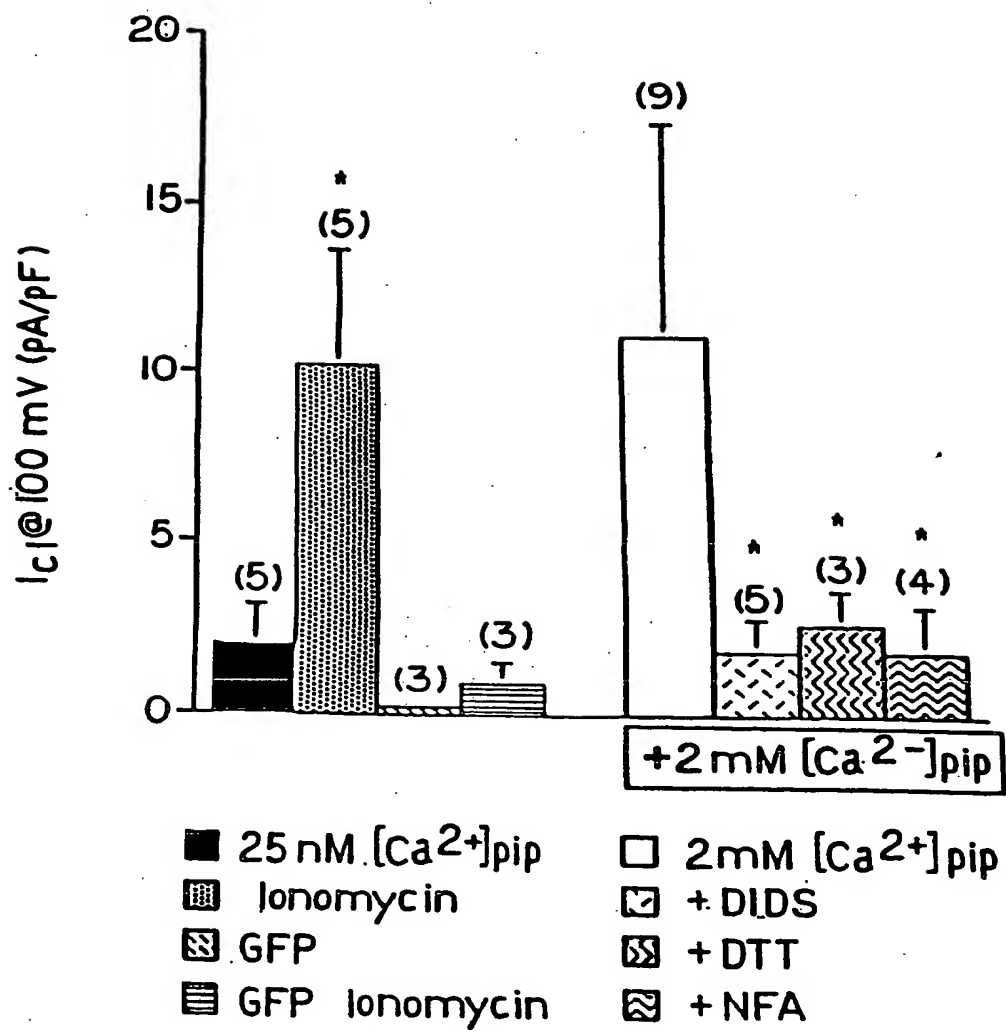
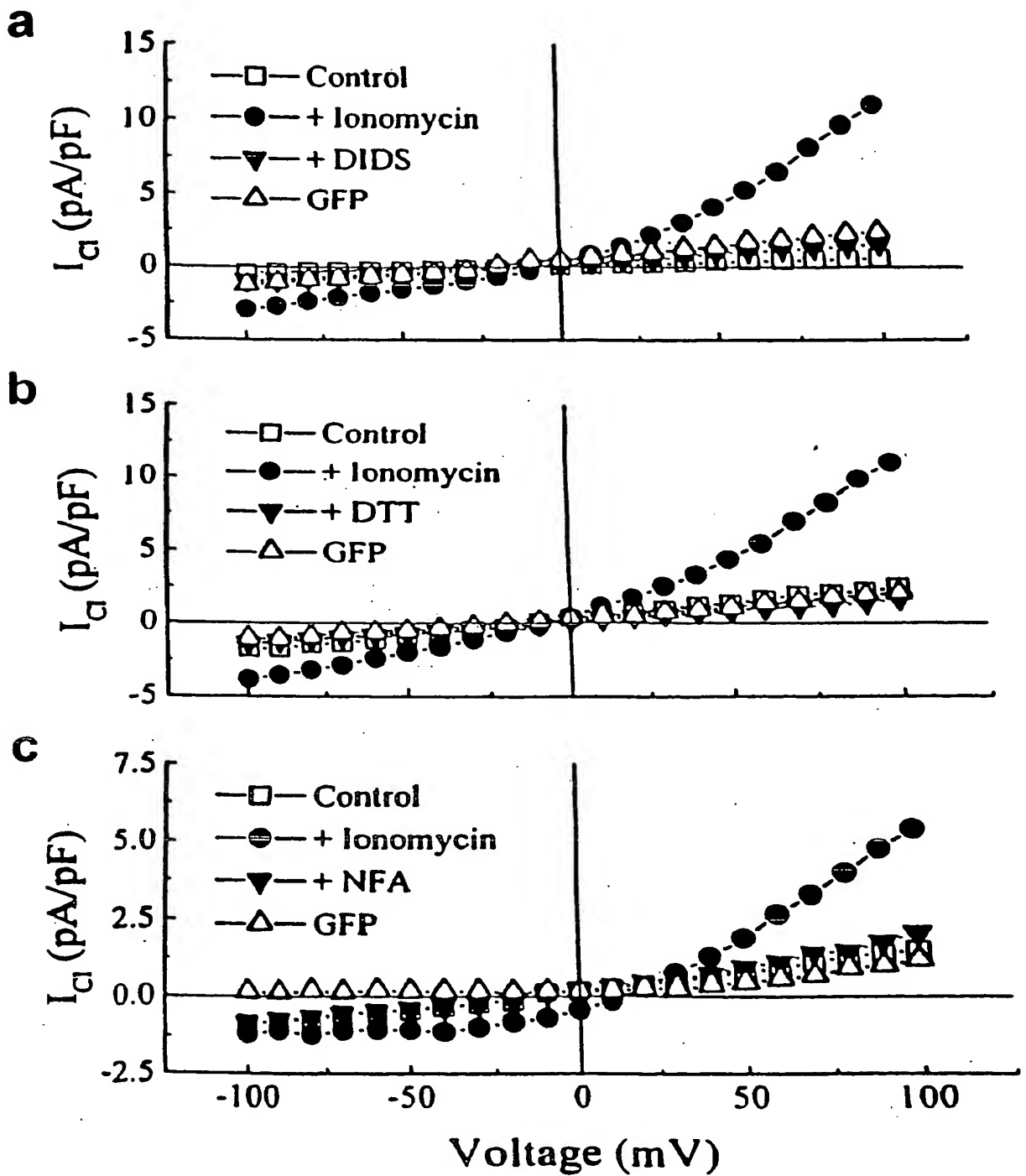


Figure 10

Fig. 11



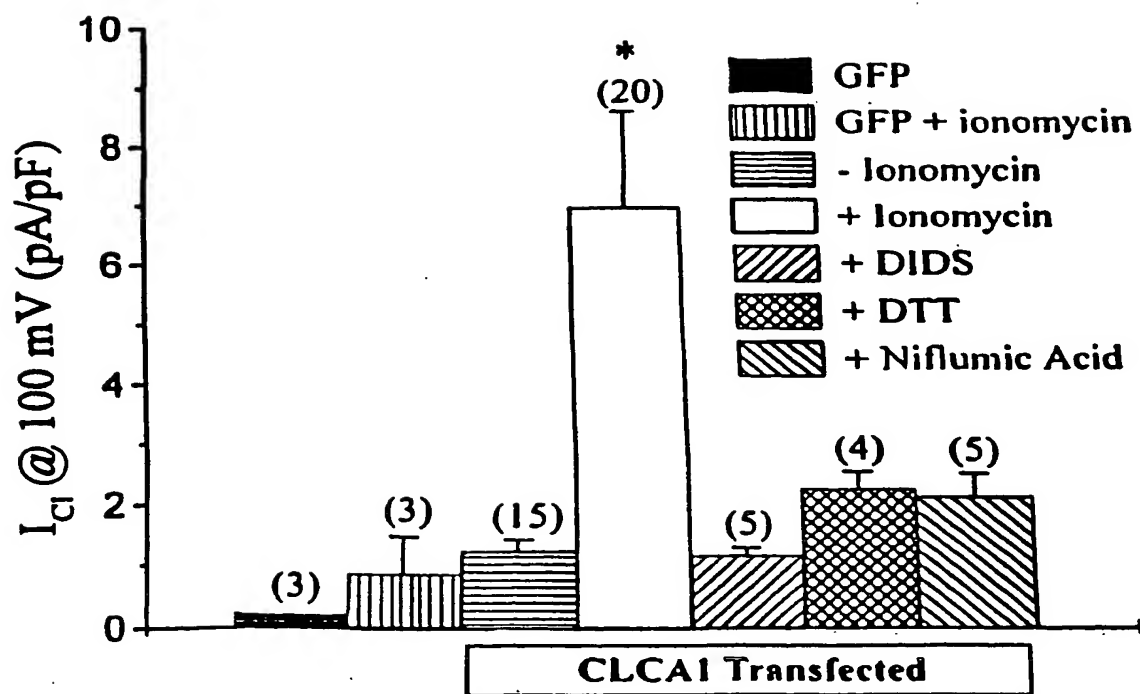
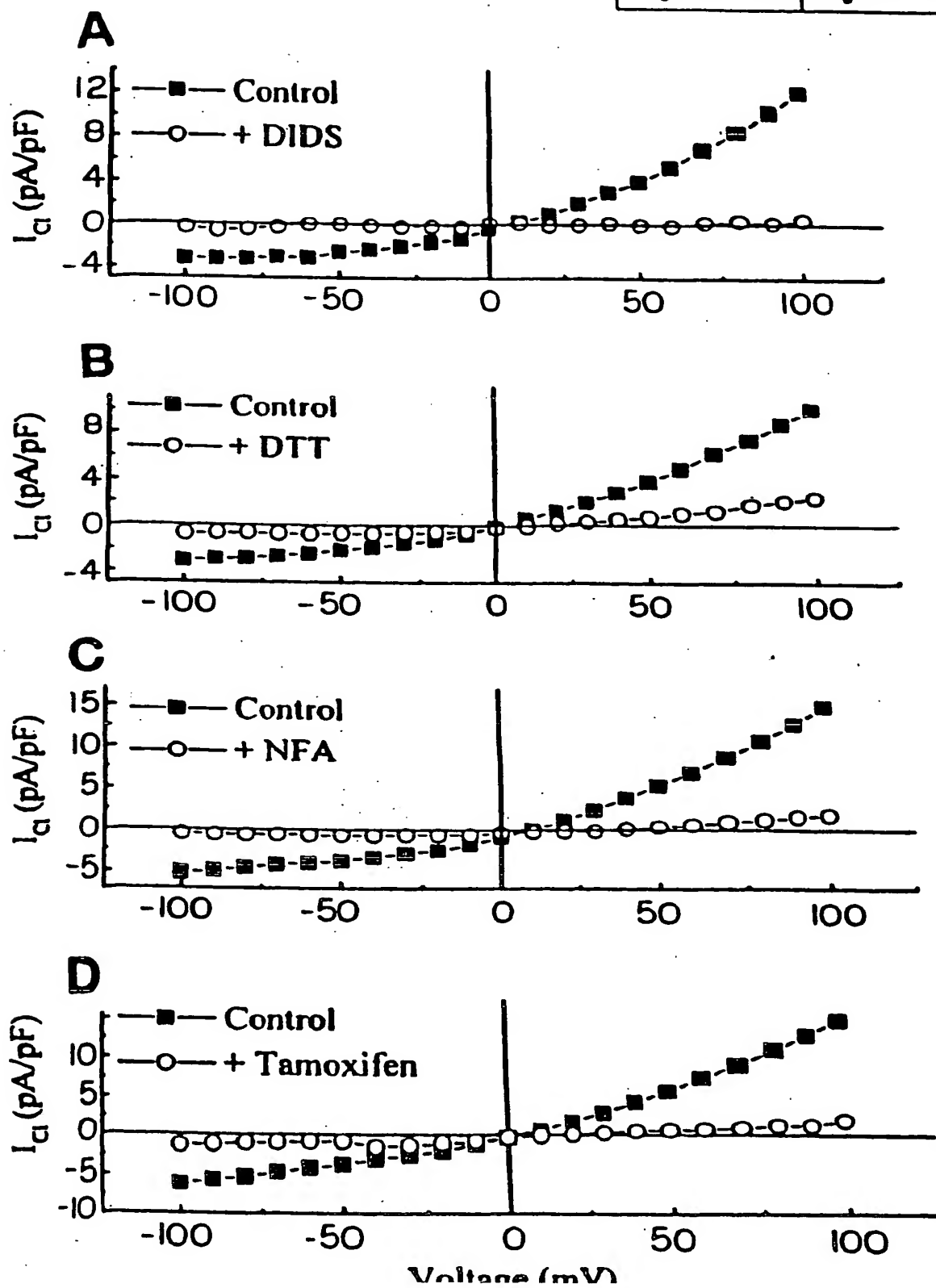


Figure 12

Figure 13

Figure 13A | Figure 13B



**E**

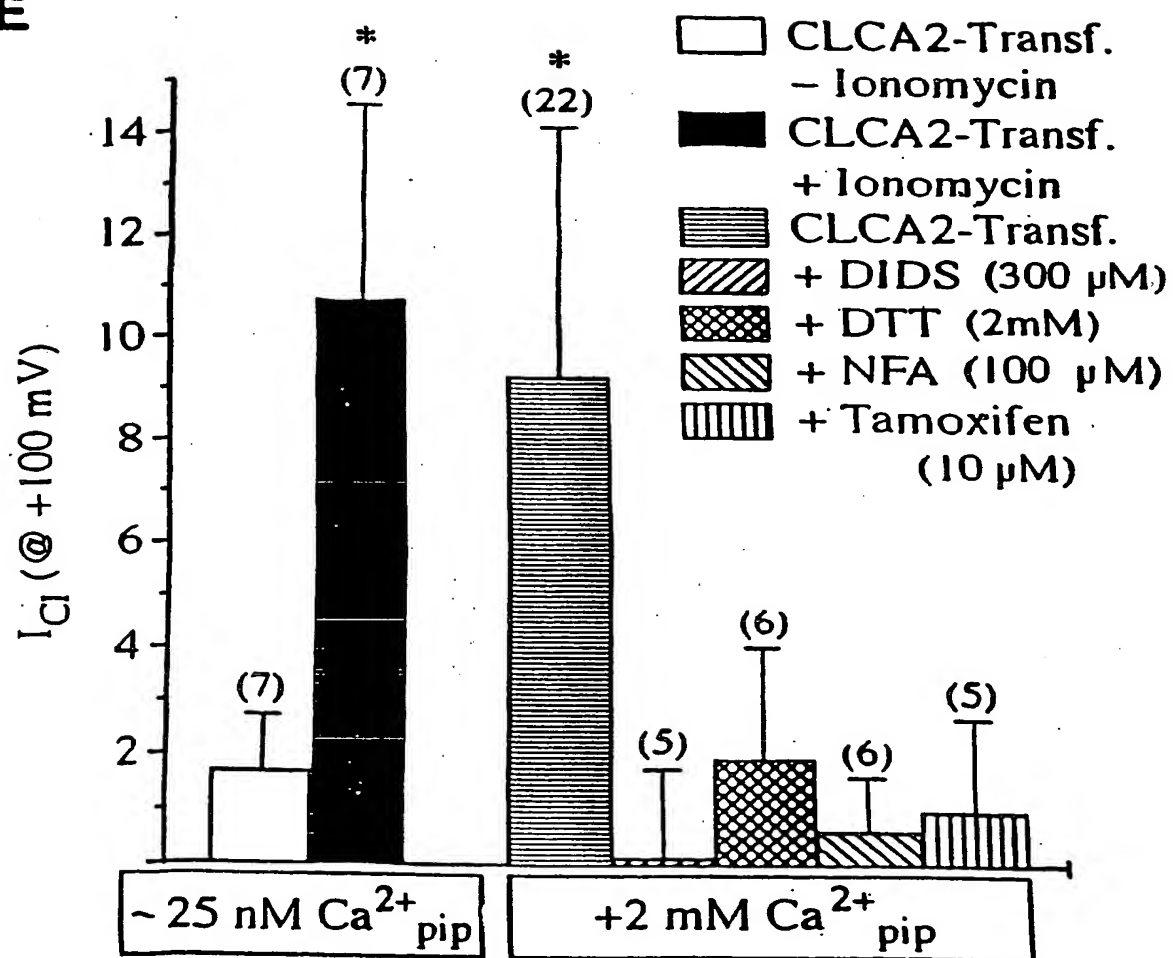


Figure 13B

## Figure 14

**Figure 14B**

h CLCA2 MTORSIAGPICNLKFVTLVALSSELPFLGAGVOLQDNGYNGLLIAINPQVPENQNLISNIKEMITEASFYLFNATKRRV 80  
 h CLCA1 .GPEKSS-----VFILI.HL-.EGA.S--NSLI..NN..E.IVV.D.N..DET.QQ.D.V.Q..L...E..GK.F 72  
 b CLCA1 .VP.LTV-----IL.L.HL-.PG-MK--SSM.N.IN..D.IV....S..DEK.Q....V...T...H..... 71  
 Lu-ECAM-1 .VLCLNV-----IL.L.HL-.PG-MK--SSM.N.IN..D.IV....S..DEK.E....V...T...H..... 71  
 m CLCA1 .VPGLV-----L.L.HL-.QN-TE--SSM.H.NS..E.VV....S..DER.PS....V.Q..T...E.SQG.. 71  
  
 h CLCA2 FFRNIKILIPATWKANN-SKIKQESYEKANVIVTDWYGAHGDDPYTLQYRGCCKEGKGYIHFTPNFLNDNLTAGYSGRG 159  
 h CLCA1 Y.K.VA...E...TKADYVRP.L.T.KN.D.L.AESTPPGN.E..E.MGN.EK.ER..L..D.IAGKK.AE-..PQ. 151  
 b CLCA1 Y...VS...M...SKSEYLP...DQ.E...ANP.LK....GR.EK.Q....TN..PI-... 150  
 Lu-ECAM-1 Y...VS...M...SKSEYFIP...DQ.D...ANP.LKY....GR.EK....TN.FHI-... 150  
 m CLCA1 Y...S.V.M...SKSEYLP.R...D.D...A.PHLQ....GQ.DR.Q....T...RI-..P... 150  
  
 h CLCA2 RVFVHEWAHLRWGVFDEYNNDKPFYINGONQIKVTRCSSDITGIFV---CEKGPQPCQENCIISK---LFKEGCTFIYNS 232  
 h CLCA1 KA.....EK..LS-NGR.QAV...AG...TN.V-KK.QG.S.YTKR.TFN.VTG.YEK...E.VLQ. 229  
 b CLCA1 .A.....I.....G.Q....SRR.T.EA...TH...TN.IVK-QG.S.ITRP.RRDSQTG.YEAK...PEK 229  
 Lu-ECAM-1 .....I.....V.Q....SRK.T.EA...TH...N.VFKK.PG.S.ITSL.RRDSQTG.YEAK...LPKK 230  
 m CLCA1 .....V.R....SRK.T.EA...AS...KK.V-HE.QR.S.VTRA.RRDSKTR.YEPK...PDK 229  
  
 h CLCA2 TQONATASIMFMQSLSSVVEFCNASTHNQEAAPNLQNMCMCLRSANDVITDSADFHHSFPMNGTLPPTFSLVQAGDKVV 312  
 h CLCA1 R.TEK...A.HVD.I...TEQN.K...K.N...T.E.R.E.KKT..TT--Q.N...L.I.QRI. 307  
 b CLCA1 S.T.RE...H...T...TEK..V.....K.KNGK.T...MN.T.QNTS..TEMNP.TQ....LKSQR.. 309  
 Lu-ECAM-1 S.T.KE...P.H...T...TEK..T...K.KNGK.T...MN.V.QNTS..TEMNP.TH....LKSQR.. 310  
 m CLCA1 I.T.G.....N.N.....TENN.A.....K.NR..T...KT....QNA.P.R...A....Y.LKSRRR.. 309  
  
 h CLCA2 CLVLVDSSKMAEADRLLOLQQAEEFYLMQIVEIHTFVGIAFSKGEIRAOHQINSNDDRKLLVSLPTTVSAKTDISI 392  
 h CLCA1 .....K.GS..TGN..NR.N..GOLF.L.T..LGSW..MVT...AAHVQSE.I...GS..DT.AKR..AA--SGGT.. 385  
 b CLCA1 .....K.GS.SSE...FRMN...LF.I..I.KGSL..MVT...VA...NN.TK.TDDNVYENITAN..QE--NGGT.. 387  
 Lu-ECAM-1 .....K.GS.SAE...F.MN...L..I.VI.KGSL..MVT...VA..QNH.TR.TDDNVYQKITAK..QV--NGGT.. 388  
 m CLCA1 .....K.GS.DKE...IRMN...L..T....KESM..LVT...AAH.QNY.IK.T.SS.YQKITAN..QQ--SGGT.. 387  
  
 h CLCA2 CSGLLKKGFEVVEKLNKAYGSVMILVTSGDDKLLGNCLFTVLSSGSTIHSIALGSSAAPNLELSRLTGLKFFVDPDISN 472  
 h CLCA1 .....RSA..-T.IRKKYPTD..EIV.L.D.E.NTISG.FNE.KQ..AI..TV...P...QE....KM....QTYAS.QVQ 464  
 b CLCA1 .....R...A..QAIIQSQSTS..E.I..L.D.E.NEIH.S.IEE.KQ..VI..T...P...KE..T.DM...HR.YANKDI- 466  
 Lu-ECAM-1 .....R...A..QAIIHSQSTS..E.I..L.D.E.NEINS.FED.KR..AI..T...P...KE..T.NM...YR..ANKDI- 467  
 m CLCA1 .....H..QA..QAITSQSTS..EIV.L.D.E.NGIRS.FEA.SR..AI..T...P.R.RE..T.DM....R.YANKDL- 466

h CLCA2	SNSMIDAFSRISSGTDIFQOHIQLESTGENVPHHQLKNTVTVDNTVGNDFMLVWTWQASGPPEILFDPGRKYYTNN	552
h CLCA1	N.GL....GAL...N.AVS.RS....K.LTLQNSQWMNG..I.S...K..L..I..-TTQ..Q.L.W..S.Q.--QGG	541
b CLCA1	-GLTN.....RS.S.T..T.....KALAITKQWNG..P.S.I....F.V....TIKK...L.Q..K.K..K.SD	544
Lu-ECAM-1	-TGLTN.....RS.S.T..A.....KALKITGRKRVNG..P.S.....F.V....TIQK...V.Q..K.K..K.SD	545
m CLCA1	-..L.....TS.SVS..AL....KAFD.RAGAWING..PL.S.....F.VI...MVKK.....Q..K.K..T.SD	544
h CLCA2	FITN-LTERTASLWIPGTAKPGHWTYTLNTHHSLOALKVTVTSRASNSAVPPATVEAFVERDSLHFPHPVMIYANVKQG	631
h CLCA1	.VVDK-NTKM.Y.Q...I..V.T.K.S---QA.S.T.TL.....ATL..I..TSKTNK.TSK..S.LVV...IR..	617
b CLCA1	.KEDK.NIHS.R.R...I.ET.T...S.L.N.A.P.I.T...T.RSPTT..V.AT.HMSQNTA.Y.S..IV..Q.S..	624
Lu-ECAM-1	.KEDK.NI.S.R.Q...I.ET.T...S.L.N.A.S.M.T...T.RSPTI..VIAT.HMSQHTA.Y.S.MIV..Q.S..	625
m CLCA1	.QDDK.NI.S.R.Q....ET.T...SY--GTKS.LITM...T.RSPTME.LLGICYMSQSTAQY.SRMIV..R.S..	622
h CLCA2	FYPILNATVTATVEPETGDPVTLRLDDGAGADVKNKNGIYSRYFFSFAANGRYSLKVHVNHSPSISTPAHSIPGSHAMY	711
h CLCA1	AS...R.S...LI.SVN.KT...E..N....AT.D.V....TTYDT....V..RALGGVNAARRRVIPQQ.G.L.	697
b CLCA1	.L.V.GIN...II.T.D.HQ...E.W.N....TV.....TDYRG.....AEARNNTARLSLQ.QNK.L.	704
Lu-ECAM-1	.L.V.GIS.I.II.T.D.HQ...E.W.N...R.TV.....TDYVG.....AQARNNTARLNLQ.QNKVL.	705
m CLCA1	.L.V.G.N...LI.A.H.HQ...E.W.N....IV.....TDYHG.....R.QAQRNKTRLSLQ-KNKSL.	701
h CLCA2	VPGYTANGNIQMNAPRKSVGRNEERKKG-FSRVSSGGFSVLG-VPAGHPDVPFPCKIIDLEA-VKVEEELTSLWTAP	788
h CLCA1	I..WIE.DE..W.P..PEINKDDVQH.QVC...T.....-ASD..NA.I..L...GQ.T.K.EIHGGSLIN.T....	776
b CLCA1	I...IE..K.IL.P..PE.KDDLAKAEIED...LT.....T.S.AP..-N..S.L.N.....KF.ED-HIQ.....	782
Lu-ECAM-1	....VE..K.IL.P..PE.KDDLAKA.IED...LT.....T.S.AP.P.N..S....S..T...KF.ED-YIQ.....	784
m CLCA1	I...VE..K.VL.P..PD.QEEAI.ATVED.N..T.....T.S.AP.D.D.AR....S.VT...EFIGD-YIH.T....	780
h CLCA2	GEDFDQGQATSYEIRMSKSLQNIQDDFNNAILVNTSKRNPQQAGIREIFTFSPQISTNGPEHQPNGETHESHRIYVAIRA	868
h CLCA1	.D.Y.H.T.HK.I..I.T.ILDLR.K..ESLQ...TALI.KE.NSE.V.L.K.ENI..-----FENGTDLFI..Q.	846
b CLCA1	ANVL.K.K.N..I..I...FLDL.K..D..T....SLK.KE..SD.N.E.K.EPFR-----IENGTFN.I.VQ.	852
Lu-ECAM-1	.NVL.K.K.N..I..I...FMDR.E..D..T....NLI.KE..SK.N.E.K.EHFR-----VENGTKF.ISVQ.	854
m CLCA1	.KVL.N.R.HR.I....QHPLDL.E....T...A.SLI.KE..SK.A.K.K.ETFK-----IANGIQL.I..Q.	850
h CLCA2	MDRNSLQSAVSNIAQAPLFIPPNSDP-VPARDYLILKGVLTANGLIICLIIVVTHHTLSRKKRADKKENGTKLL	943
h CLCA1	V.KVD.K.EI....RVS....QTP.ET.SP.-----ETSAPCPN-.H.NST.PGIHILKIMW.WIG---.LQLSIA	914
b CLCA1	INEAN.T.E.....IK...MP-----EDSVP.L.-TK.SAINLAIFALAMI-----LSIV.	904
Lu-ECAM-1	INEAN.I.E..H.V..IK...LP-----EDSVHDL.-TK.SEITLAILGLPMI-----FSV-F	905
m CLCA1	DNEA..T.E.....VKLTSL-----EDSIS.L.-DD.SAISMTINGL.VI-----FNSI.N	902

Figure 14B

Fig. 15A

# GST-bCLCA2 Fusion Proteins

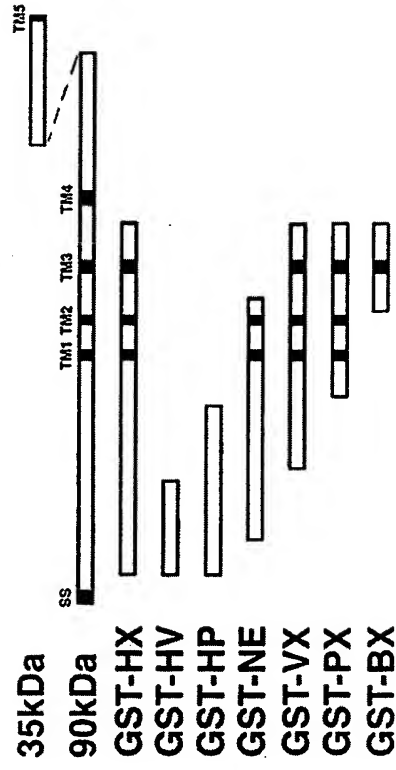


Fig. 15C

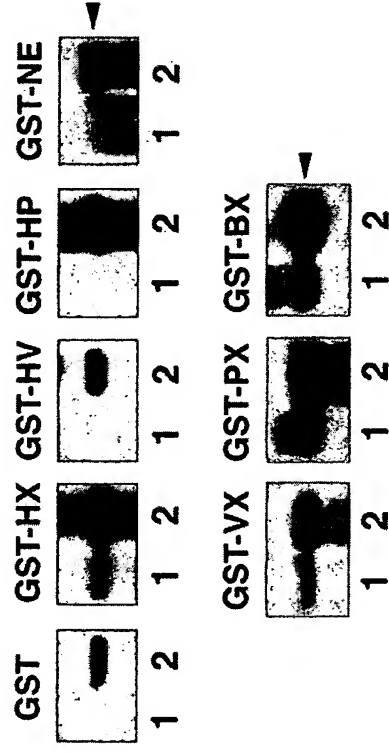


Fig. 15B

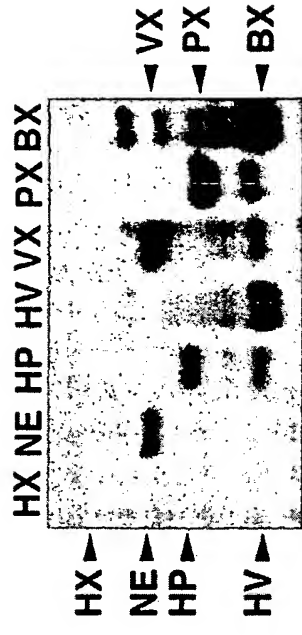


Fig. 15D

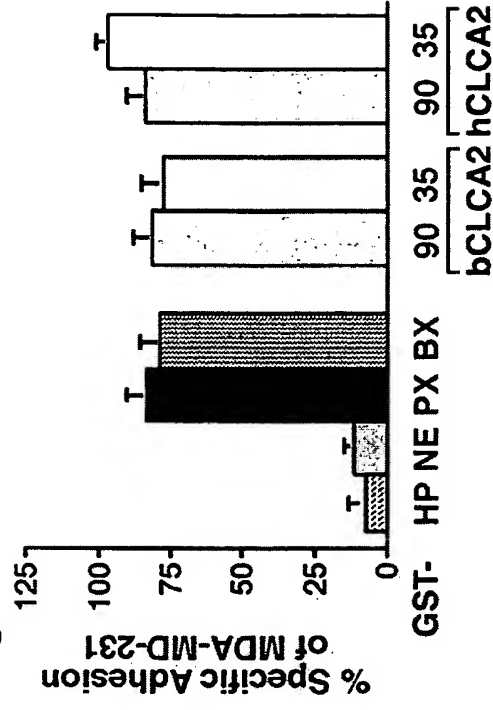




Fig. 16A

	90-kDa	35-kDa
hCLCA2	AFSRISSGTG	GFSRVSSGGG
mCLCA5	AFVRISSGTG	GFSRVSSGGG
mCLCA1	AFSRISSSTG	DFNRVTSGGG
bCLCA2	AFSRISSRRSG	DFSRLTSGGG

Fig. 16B

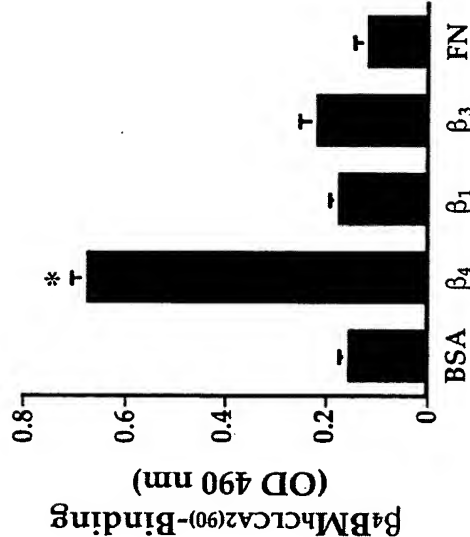


Fig. 16C

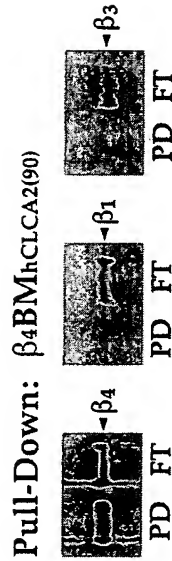


Fig. 16D



Fig. 17A

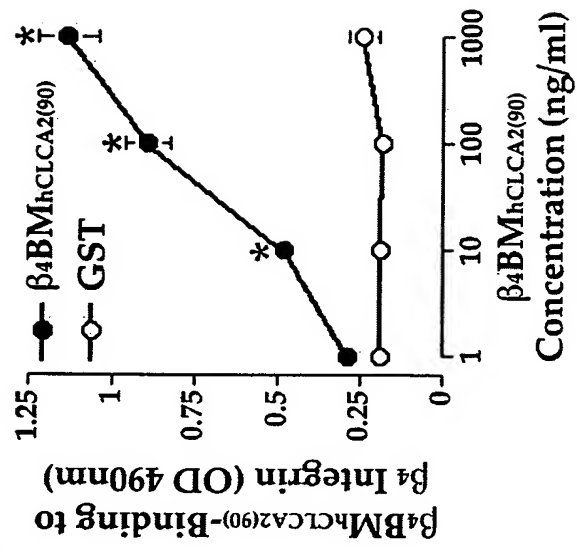


Fig. 17B

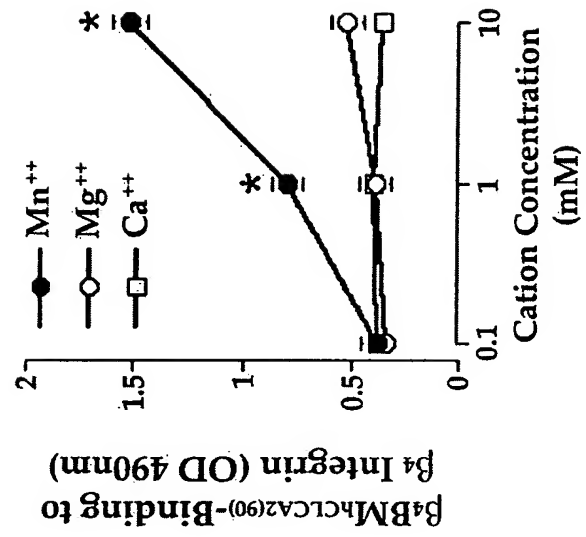


Fig. 17A

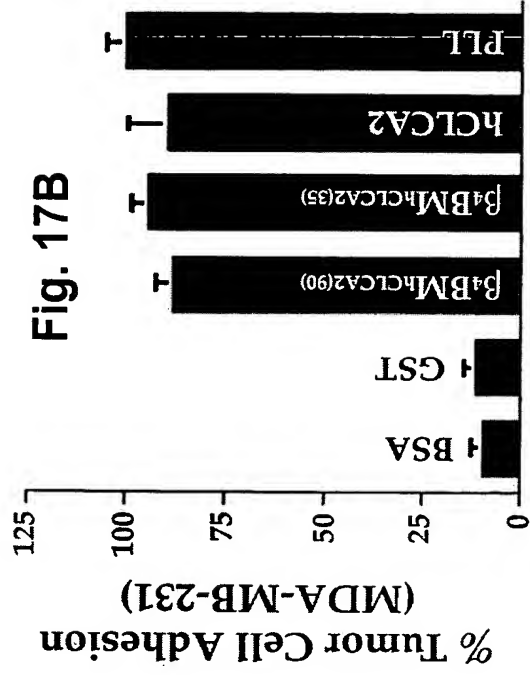
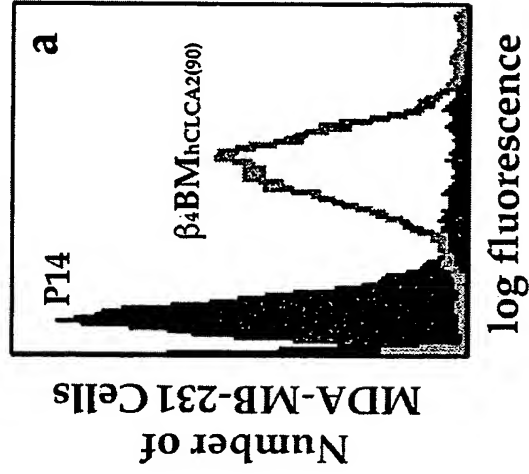
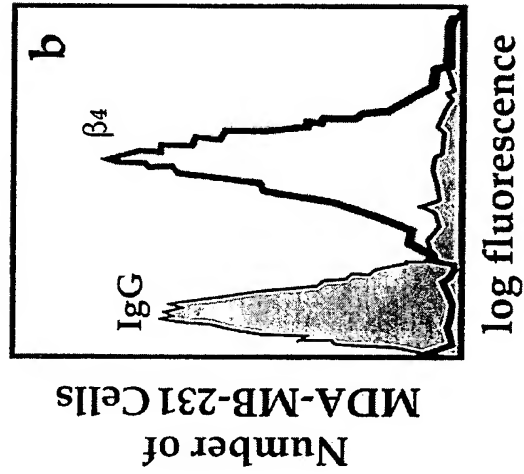
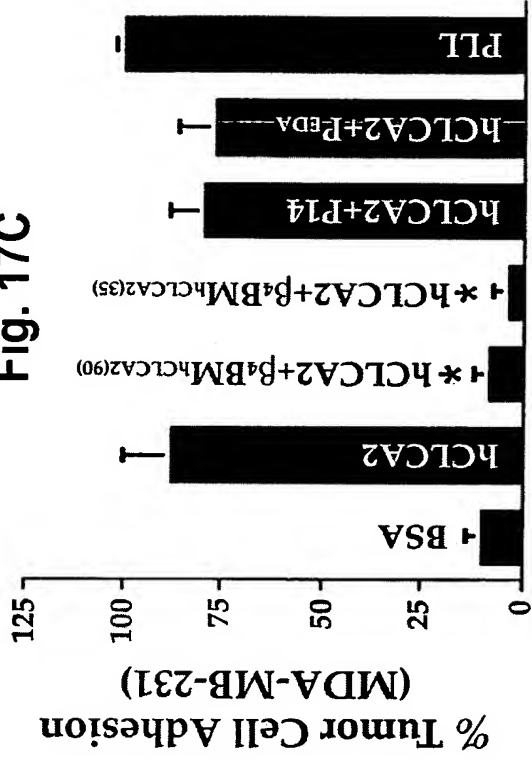
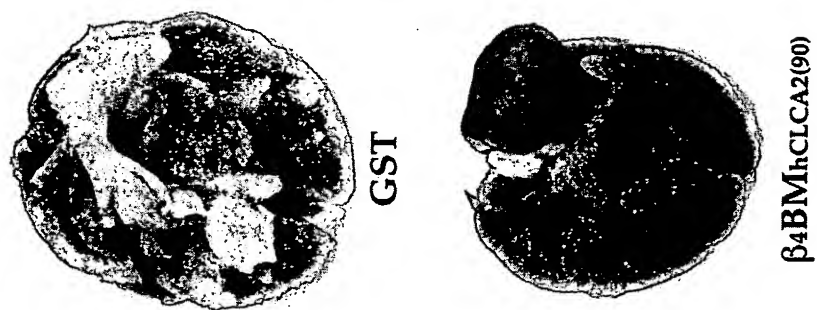
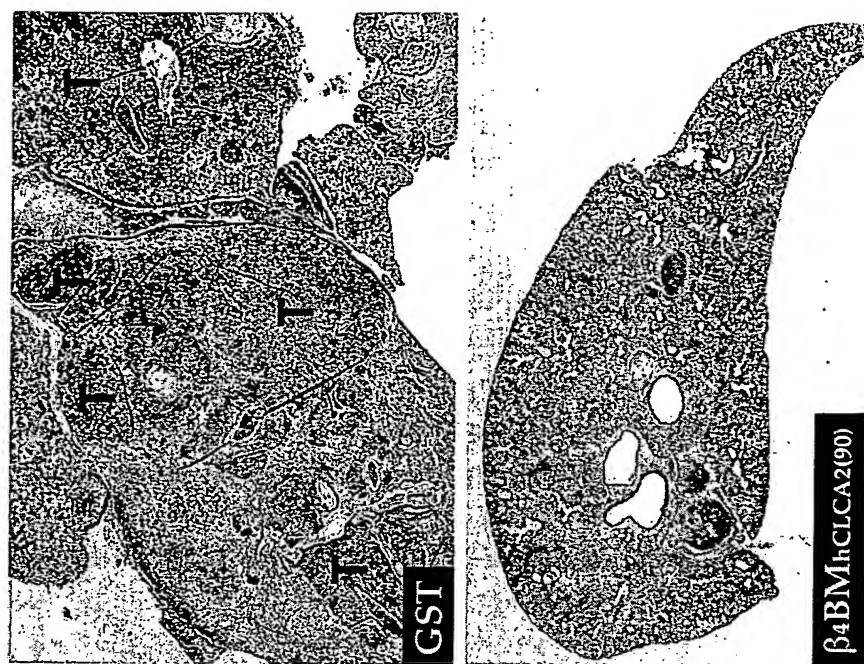
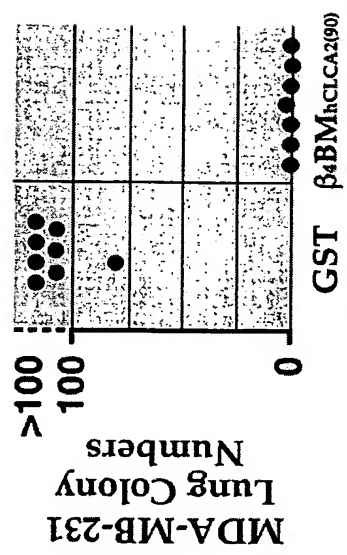


Fig. 17C





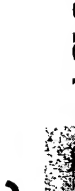
**Fig. 19B**

27	111 184-203	343	711 733	1752
----	-------------	-----	---------	------

PS\*  
 EEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  
 KTUMPYIS-TTPAKLRPCTSEQNCTTFFSYXNVLSTNK 228  
 KVSVPQOTDM-RPEKLEP--WPNS-DPPFSXKNVISLTD 212

\* Predicted Secondary Structure: E, sheet; C, coil. (see ref. 27)

**Fig. 20C**

  
GST-β<sub>1</sub> GST-β<sub>4</sub> hCLCA2 hCLCA2 in Lysate

Well Coating (4°C)	hCLCA2 Binding (OD 490nm)
None	~0.85
BSA	~0.15
BSA + hCLCA2	~0.60

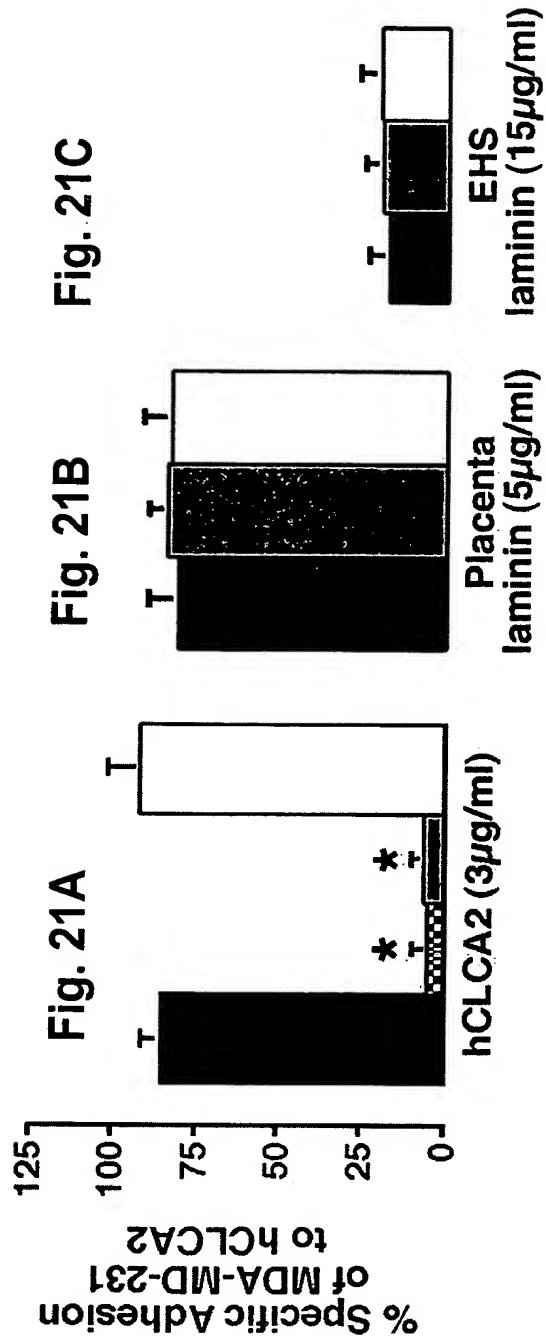
hCLCA2 (3μg/ml)  
GST (10μg/ml; o.n.),  
then hCLCA2 (2h)  
GST-β1 (10μg/ml; o.n.),  
then hCLCA2 (2h)  
GST-β4 (10μg/ml; o.n.),  
then hCLCA2 (2h)

Condition	GST- $\beta_4$ Binding (OD 490nm)
Milk	~0.15
$\beta_4$ BMhCtCAZ(90)	~0.85
PEDA	~0.10

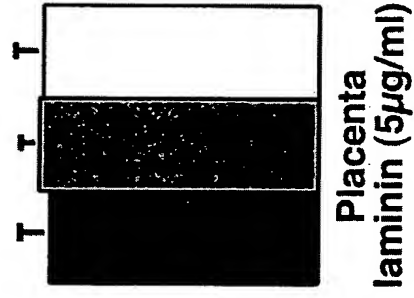
WB:  $\alpha$ -Myc

IP:  $\alpha 6$   $\beta 4$   $\beta 4.1-4$   $\beta 4.1-4$

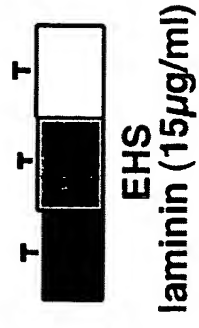
hCLCA2



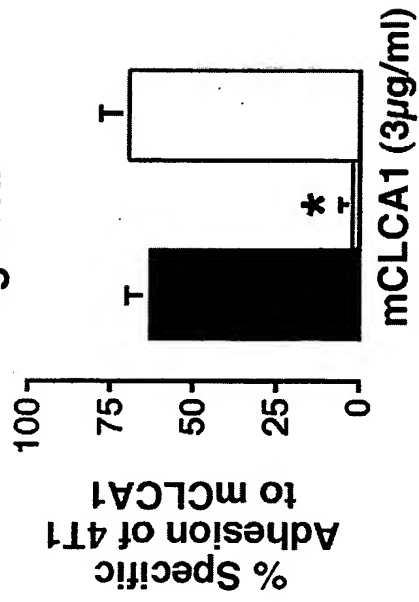
**Fig. 21B**



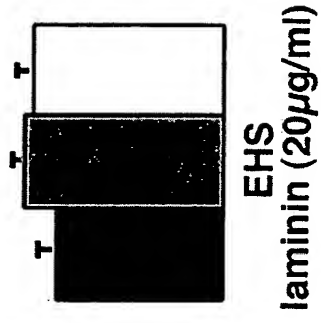
**Fig. 21C**



**Fig. 21D**



**Fig. 21E**



■ Substrate alone   
 ■ in the presence of  $\beta_4$ -peptide   
 ■ blocked with  $\beta_1$ -peptide   
 ■ blocked with  $\beta_4$ -peptide

Fig. 22A



Fig. 22B

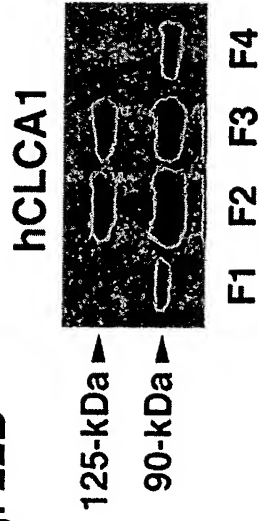


Fig. 22D

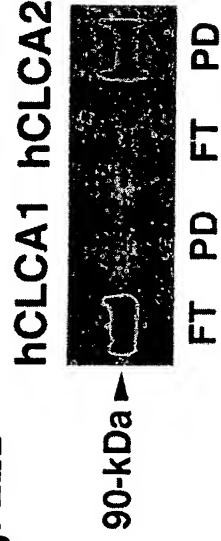


Fig. 22C

